

### AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

#### LISTING OF CLAIMS

1.-35. (Canceled)

36. (Original) A method for identifying a compound which binds to a preselected biomolecular target, said compound being present in a mixture of compounds comprising:

(a) providing a complex of said biomolecular target and a standard binding compound which binds to said target under conditions effective to achieve said binding;

(b) combining with said complex under competitive binding conditions the mixture of compounds;

(c) ionizing said combination in a mass spectrometer to provide a plurality of ions;

(d) fragmenting at least one of said ions in a mass spectrometer, (e) collecting mass spectral data for the fragmentation; and

(f) relating said mass spectral data to the existence and degree of competitive binding.

37. (Original) The method of claim 36 wherein said biomolecular target is a nucleic acid.

38. (Original) The method of claim 37 wherein said nucleic acid is RNA.

39. (Original) The method of claim 38 wherein said RNA includes one or more deoxynucleotides at preselected locations thereof.

40. (Canceled)

41. (Original) A method for identifying a compound which binds to a preselected biomolecular target, said compound being present in a mixture of compounds comprising:

(a) providing a complex of said biomolecular target and a standard compound which binds to said target under conditions effective to achieve said binding;

(b) acquiring fragmentation data from the mass spectrometric analysis of the complex;

(c) combining with a further portion of said complex under competitive binding conditions the mixture of compounds;

(d) ionizing said combination in a mass spectrometer to provide a plurality of ions;

(e) fragmenting at least one of said ions in a mass spectrometer;

(f) collecting mass spectral data for the fragmentation; and (g) relating the mass spectral data acquired in steps (b) and (f) to the existence and degree of competitive binding of said compound.

42. (Original) A method for identifying in a combinatorial mixture compounds which bind to a biomolecular target, wherein the method comprises:

(a) providing mass spectral data on the ion abundance for said biomolecular target;

(b) providing a first complex of said biomolecular target and a standard binding compound which binds to said target;

(c) combining with said first complex a combinatorial mixture of compounds;

(d) ionizing in a mass spectrometer said combination from step {circle over (c)} to provide a plurality of ions for said combination;

(e) collecting from the ionization of step (d) mass spectral data on the ion abundance of said first complex, wherein said ion abundances in steps (a) and (e) affords information for effecting said determination.

43. (Original) The method of claim 42 wherein mass differences in the mass spectral data from steps (a) and (e) are identified for determining the mass of compounds from the combinatorial mixture which preferentially bind with said bimolecular target.

44. (Original) The method of claim 42 wherein said biomolecular target is a nucleic acid.

45. (Original) The method of claim 44 wherein said nucleic acid is RNA.

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46. (Original) The method of claim 45 wherein said RNA corresponds to a 16S rRNA A-site.

47. (Original) The method of claim 45 wherein said RNA includes one or more deoxynucleotide subunits at preselected locations thereof.

48. - 94. (Canceled)

95. (New) The method of claim 36, wherein said compound is an oligonucleotide.

96. (New) The method of claim 38 wherein said RNA comprises at least one mismatched base pair, loop, bulge, kink, or stem structure.

97. (New) The method of claim 38, wherein said compound is a small molecule.

98. (New) The method of claim 38, wherein said RNA comprises a molecular interaction site present in two or more distinct taxonomic species.

99. (New) The method of claim 41, wherein said compound is an oligonucleotide.

100. (New) The method of claim 41, wherein said biomolecular target is a nucleic acid.

101. (New) The method of claim 100, wherein said nucleic acid is RNA.

102. (New) The method of claim 101, wherein said RNA comprises at least one mismatched base pair, loop, bulge, kink, or stem structure.

103. (New) The method of claim 101, wherein said RNA comprises a molecular interaction site present in two or more distinct taxonomic species.

104. (New) The method of claim 100, wherein said compound is a small molecule.

105. (New) The method of claim 42, wherein said compound is an oligonucleotide.

106. (New) The method of claim 45, wherein said RNA comprises at least one mismatched base pair, loop, bulge, kink, or stem structure.

107. (New) The method of claim 45, wherein said RNA comprises a molecular interaction site present in two or more distinct taxonomic species.

108. (New) The method of claim 45, wherein said compound is a small molecule.